0590
0731

#6

OIPE

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RAW SEQUENCE LISTING              DATE: 07/05/2001
PATENT APPLICATION:  US/09/602,740   TIME: 11:39:12

     Input Set : D:\seqlistcorr.txt
     Output Set: N:\CRF3\07052001\I602740.raw
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 3 <110> APPLICANT: Pompejus, Markus
 4         Kroger, Burkhard
 5         Schroder, Hartwig
 6         Zelder, Oskar
 7         Haberhauer, Gregor
 9 <120> TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
10         INVOLVED IN CARBON METABOLISM AND ENERGY
11         PRODUCTION
13 <130> FILE REFERENCE: BGI-126CP
15 <140> CURRENT APPLICATION NUMBER: US 09/602,740
16 <141> CURRENT FILING DATE: 2001-06-20
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19 <151> PRIOR FILING DATE: 1999-06-25
21 <150> PRIOR APPLICATION NUMBER: 60/143,208
22 <151> PRIOR FILING DATE: 1999-07-09
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25 <151> PRIOR FILING DATE: 1999-08-31
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40 <151> PRIOR FILING DATE: 1999-07-08
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60 <150> PRIOR APPLICATION NUMBER: DE 19931634.1
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64 <151> PRIOR FILING DATE: 1999-07-09
66 <150> PRIOR APPLICATION NUMBER: DE 19932227.9
67 <151> PRIOR FILING DATE: 1999-07-09
69 <150> PRIOR APPLICATION NUMBER: DE 19932230.9
70 <151> PRIOR FILING DATE: 1999-07-09
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C--> (line 16 marked)

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see page 5

RAW SEQUENCE LISTING   DATE: 07/05/2001
PATENT APPLICATION: US/09/602,740   TIME: 11:39:12

Input Set : **D:\seqlistcorr.txt**
Output Set: **N:\CRF3\07052001\I602740.raw**

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96  <150> PRIOR APPLICATION NUMBER: DE 19942088.2
97  <151> PRIOR FILING DATE: 1999-09-03
99  <150> PRIOR APPLICATION NUMBER: DE 19942095.5
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102 <150> PRIOR APPLICATION NUMBER: DE 19942123.4
103 <151> PRIOR FILING DATE: 1999-09-03
105 <150> PRIOR APPLICATION NUMBER: DE 19942125.0
106 <151> PRIOR FILING DATE: 1999-09-03
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111 <211> LENGTH: 828
112 <212> TYPE: DNA
113 <213> ORGANISM: Corynebacterium glutamicum
115 <220> FEATURE:
116 <221> NAME/KEY: CDS
117 <222> LOCATION: (101)..(805)
118 <223> OTHER INFORMATION: RXS02735
120 <400> SEQUENCE: 1
121 gaggagcttc gccacatgga tccagatttg ggctaccagc acgcactatc cggcttgtcc 60
123 agcgtcaagc tggaaaccgt ctaaggagaa atacaacact atg gtt gat gta gta 115
124                                                 Met Val Asp Val Val
125                                                 1               5
127 cgc gca cgc gat act gaa gat ttg gtt gca cag gct gcc tcc aaa ttc 163
128 Arg Ala Arg Asp Thr Glu Asp Leu Val Ala Gln Ala Ala Ser Lys Phe
129                 10                  15                  20
131 att gag gtt gtt gaa gca gca act gcc aat aat ggc acc gca cag gta 211
132 Ile Glu Val Val Glu Ala Ala Thr Ala Asn Asn Gly Thr Ala Gln Val
133             25                  30                  35
135 gtg ctc acc ggt ggt ggc gcc ggc atc aag ttg ctg gaa aag ctc agc 259
136 Val Leu Thr Gly Gly Gly Ala Gly Ile Lys Leu Leu Glu Lys Leu Ser
137         40                  45                  50
139 gtt gat gcg gct gac ctt gcc tgg gat cgc att cat gtg ttc ttc ggc 307
140 Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile His Val Phe Phe Gly
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RAW SEQUENCE LISTING   DATE: 07/05/2001
PATENT APPLICATION: US/09/602,740   TIME: 11:39:12

Input Set : D:\seqlistcorr.txt
Output Set: N:\CRF3\07052001\I602740.raw

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141       55                    60                    65
143 gat gag cgc aat gtc cct gtc agt gat tct gag tcc aat gag ggc cag   355
144 Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu Ser Asn Glu Gly Gln
145 70                    75                    80                    85
147 gct cgt gag gca ctg ttg tcc aag gtt tct atc cct gaa gcc aac att   403
148 Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile Pro Glu Ala Asn Ile
149                    90                    95                   100
151 cac gga tat ggt ctc ggc gac gta gat ctt gca gag gca gcc cgc gct   451
152 His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala Glu Ala Ala Arg Ala
153              105                   110                   115
155 tac gaa gct gtg ttg gat gaa ttc gca cca aac ggc ttt gat ctt cac   499
156 Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn Gly Phe Asp Leu His
157          120                   125                   130
159 ctg ctc ggc atg ggt ggc gaa ggc cat atc aac tcc ctg ttc cct cac   547
160 Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn Ser Leu Phe Pro His
161          135                   140                   145
163 acc gat gca gtc aag gaa tcc tcc gca aag gtc atc gcg gtg ttt gat   595
164 Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val Ile Ala Val Phe Asp
165 150                   155                   160                   165
167 tcc cct aag cct cct tca gag cgt gca act cta acc ctt cct gcg gtt   643
168 Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu Thr Leu Pro Ala Val
169                   170                   175                   180
171 cac tcc gca aag cgc gtg tgg ttg ctg gtt tct ggt gcg gag aag gct   691
172 His Ser Ala Lys Arg Val Trp Leu Leu Val Ser Gly Ala Glu Lys Ala
173              185                   190                   195
175 gag gca gct gcg gcg atc gtc aac ggt gag cct gct gtt gag tgg cct   739
176 Glu Ala Ala Ala Ala Ile Val Asn Gly Glu Pro Ala Val Glu Trp Pro
177          200                   205                   210
179 gct gct gga gct acc gga tct gag gaa acg gta ttg ttc ttg gct gat   787
180 Ala Ala Gly Ala Thr Gly Ser Glu Glu Thr Val Leu Phe Leu Ala Asp
181          215                   220                   225
183 gat gct gca gga aat ctc taagcagcgc cagctctaac aag                 828
184 Asp Ala Ala Gly Asn Leu
185 230                   235
188 <210> SEQ ID NO: 2
189 <211> LENGTH: 235
190 <212> TYPE: PRT
191 <213> ORGANISM: Corynebacterium glutamicum
193 <400> SEQUENCE: 2
194 Met Val Asp Val Val Arg Ala Arg Asp Thr Glu Asp Leu Val Ala Gln
195   1                    5                    10                   15
197 Ala Ala Ser Lys Phe Ile Glu Val Val Glu Ala Ala Thr Ala Asn Asn
198              20                    25                    30
200 Gly Thr Ala Gln Val Val Leu Thr Gly Gly Gly Ala Gly Ile Lys Leu
201          35                    40                    45
203 Leu Glu Lys Leu Ser Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile
204      50                    55                    60
206 His Val Phe Phe Gly Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu
207 65                    70                    75                    80
```

```
209 Ser Asn Glu Gly Gln Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile
210             85                  90                  95
212 Pro Glu Ala Asn Ile His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala
213            100                 105                 110
215 Glu Ala Ala Arg Ala Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn
216         115                 120                 125
218 Gly Phe Asp Leu His Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn
219     130                 135                 140
221 Ser Leu Phe Pro His Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val
222 145                 150                 155                 160
224 Ile Ala Val Phe Asp Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu
225             165                 170                 175
227 Thr Leu Pro Ala Val His Ser Ala Lys Arg Val Trp Leu Leu Val Ser
228             180                 185                 190
230 Gly Ala Glu Lys Ala Glu Ala Ala Ala Ala Ile Val Asn Gly Glu Pro
231         195                 200                 205
233 Ala Val Glu Trp Pro Ala Ala Gly Ala Thr Gly Ser Glu Glu Thr Val
234     210                 215                 220
236 Leu Phe Leu Ala Asp Asp Ala Ala Gly Asn Leu
237 225                 230                 235
240 <210> SEQ ID NO: 3
241 <211> LENGTH: 468
242 <212> TYPE: DNA
243 <213> ORGANISM: Corynebacterium glutamicum
245 <220> FEATURE:
246 <221> NAME/KEY: CDS
247 <222> LOCATION: (101)..(445)
248 <223> OTHER INFORMATION: RXA01626
250 <400> SEQUENCE: 3
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253 acattaccgt ctgaaaaatt tcatccgtag gctaagagc atg tcg aaa acg atc   115
254                                             Met Ser Lys Thr Ile
255                                             1               5
257 atc gtg cgc acc gaa att gaa atc cct gga cac cca acc gcc atc cat 163
258 Ile Val Arg Thr Glu Ile Glu Ile Pro Gly His Pro Thr Ala Ile His
259             10                  15                  20
261 atc gca gag atg cag gag ctt ccc cca tct gag gct caa ggc ggc gtg 211
262 Ile Ala Glu Met Gln Glu Leu Pro Pro Ser Glu Ala Gln Gly Gly Val
263             25                  30                  35
265 cag atg tgc aaa atg cag cgc att att gaa cta gca gga act gcc gaa 259
266 Gln Met Cys Lys Met Gln Arg Ile Ile Glu Leu Ala Gly Thr Ala Glu
267         40                  45                  50
269 ggg gat gtc gtt act ggt gca ggt gtt att ggc gga tct aat ttc cag 307
270 Gly Asp Val Val Thr Gly Ala Gly Val Ile Gly Gly Ser Asn Phe Gln
271     55                  60                  65
273 ctg aat aac gag cca aat gaa gtg gtt ccc cat cca gat acc tat gcg 355
274 Leu Asn Asn Glu Pro Asn Glu Val Val Pro His Pro Asp Thr Tyr Ala
275 70                  75                  80                  85
277 gat ttc ccc gat atc aag gcg gtt gtt atc tcc gcg gag act ttt gaa 403
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RAW SEQUENCE LISTING   DATE: 07/05/2001
PATENT APPLICATION: US/09/602,740   TIME: 11:39:12

Input Set : D:\seqlistcorr.txt
Output Set: N:\CRF3\07052001\I602740.raw

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278 Asp Phe Pro Asp Ile Lys Ala Val Val Ile Ser Ala Glu Thr Phe Glu
279             90.              95              100
281 ggc ctg tgg ctg gaa gcg gga gcg aag ttc cct ggg tta aat        445
282 Gly Leu Trp Leu Glu Ala Gly Ala Lys Phe Pro· Gly Leu Asn
283             105              110              115
285 taaccacttg cagtataccc tag                                      468
288 <210> SEQ ID NO: 4
289 <211> LENGTH: 115
290 <212> TYPE: PRT
291 <213> ORGANISM: Corynebacterium glutamicum
293 <400> SEQUENCE: 4
294 Met Ser Lys Thr Ile Ile Val Arg Thr Glu Ile Glu Ile Pro Gly His
295   1               5              10               15
297 Pro Thr Ala Ile His Ile Ala Glu Met Gln Glu Leu Pro Pro Ser Glu
298             20              25               30
300 Ala Gln Gly Gly Val Gln Met Cys Lys Met Gln Arg Ile Ile Glu Leu
301         35              40              45
303 Ala Gly Thr Ala Glu Gly Asp Val Val Thr Gly Ala Gly Val Ile Gly
304     50              55              60
306 Gly Ser Asn Phe Gln Leu Asn Asn Glu Pro Asn Glu Val Val Pro His
307 65              70              75               80
309 Pro Asp Thr Tyr Ala Asp Phe Pro Asp Ile Lys Ala Val Val Ile Ser
310             85              90               95
312 Ala Glu Thr Phe Glu Gly Leu Trp Leu Glu Ala Gly Ala Lys Phe Pro
313             100             105             110
315 Gly Leu Asn
316         115
319 <210> SEQ ID NO: 5
320 <211> LENGTH: 780
321 <212> TYPE: DNA
322 <213> ORGANISM: Corynebacterium glutamicum
324 <220> FEATURE:
325 <221> NAME/KEY: CDS
326 <222> LOCATION: (101)..(757)
327 <223> OTHER INFORMATION: RXA02245
329 <400> SEQUENCE: 5
330 gccacaccgc cacggcaccg atgcgatgtt tgtggcagtg ctgcgaaaga agtagacctg 60
332 tgagctaagt ggggtagaca agagggctat gatttagggc atg gca caa cgt act 115
333                                             Met Ala Gln Arg Thr
334                                             1               5
336 cca cta atc gcc cca tcc att ctt gct gct gat ttc tcc cgc tta ggg 163
337 Pro Leu Ile Ala Pro Ser Ile Leu Ala Ala Asp Phe Ser Arg Leu Gly
338             10              15              20
340 gag cag gtg ttg gct gtt cct gat gct gac tgg att cac gtc gac atc 211
341 Glu Gln Val Leu Ala Val Pro Asp Ala Asp Trp Ile His Val Asp Ile
342             25              30              35
344 atg gac gga cac ttc gtt cca aac ttg agc ttt ggc gcg gat atc aca 259
345 Met Asp Gly His Phe Val Pro Asn Leu Ser Phe Gly Ala Asp Ile Thr
346         40              45              50
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FYI'

VERIFICATION SUMMARY   DATE: 07/05/2001
PATENT APPLICATION: US/09/602,740   TIME: 11:39:13

Input Set : **D:\seqlistcorr.txt**
Output Set: **N:\CRF3\07052001\I602740.raw**

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:9604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:107
L:57063 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:655
L:57064 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:655
L:57098 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:656